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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/869,176

DATE: 12/23/2002

TIME: 14:07:24

Input Set : A:\Ocrs3072.app

Output Set: N:\CRF4\12232002\I869176.raw

3 <110> APPLICANT: TUMER, NILGUN E.
 4 DINMAN, JONATHAN D.
 5 HUDAK, KATALIN A.
 7 <120> TITLE OF INVENTION: VIRUS-RESISTANT TRANSGENIC PLANTS
 9 <130> FILE REFERENCE: OCIRS 3.3-072
 11 <140> CURRENT APPLICATION NUMBER: 09/869,176
 12 <141> CURRENT FILING DATE: 2001-06-26
 14 <150> PRIOR APPLICATION NUMBER: 60/115,791
 15 <151> PRIOR FILING DATE: 1998-12-31
 17 <150> PRIOR APPLICATION NUMBER: PCT/US99/31312
 18 <151> PRIOR FILING DATE: 1999-12-30
 20 <160> NUMBER OF SEQ ID NOS: 14
 22 <170> SOFTWARE: PatentIn Ver. 2.1
 24 <210> SEQ ID NO: 1
 25 <211> LENGTH: 1164
 26 <212> TYPE: DNA
 27 <213> ORGANISM: Saccharomyces cerevisiae
 29 <220> FEATURE:
 30 <221> NAME/KEY: CDS
 31 <222> LOCATION: (1)..(1161)
 33 <400> SEQUENCE: 1

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36	1 5 10 15	
38	ttg cca aga aag aga gct gcc tcc atc aga gct aga gtt aag gct ttt	96
39	Leu Pro Arg Lys Arg Ala Ala Ser Ile Arg Ala Arg Val Lys Ala Phe	
40	20 25 30	
42	cca aag gat gac aga tcc aag cca gtt gct cta act tcc ttc ttg ggt	144
43	Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly	
44	35 40 45	
46	tac aag gct ggt atg acc acc att gtc aga gat ttg gac aga cca ggt	192
47	Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly	
48	50 55 60	
50	tct aag ttc cac aag cgt gaa gtt gtc gaa gct gtc acc gtt gtt gac	240
51	Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp	
52	65 70 75 80	
54	act cca cca gtt gtc gtt gtt ggt gtt gtc ggt tac gtc gaa acc cca	288
55	Thr Pro Pro Val Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro	
56	85 90 95	
58	aga ggt ttg aga tct ttg acc acc gtc tgg gct gaa cat ttg tct gac	336
59	Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp	
60	100 105 110	
62	gaa gtc aag aga aga ttc tac aag aac tgg tac aag tct aag aag aag	384

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64      115      120      125
66 gct ttc acc aaa tac tct gcc aag tac gct caa gat ggt gct ggt att 432
67 Ala Phe Thr Lys Tyr Ser Ala Lys Tyr Ala Gln Asp Gly Ala Gly Ile
68      130      135      140
70 gaa aga gaa ttg gct aga atc aag aag tac gct tcc gtc gtc aga gtt 480
71 Glu Arg Glu Leu Ala Arg Ile Lys Lys Tyr Ala Ser Val Val Arg Val
72 145      150      155      160
74 ttg gtc cac act caa atc aga aag act cca ttg gct caa aag aag gct 528
75 Leu Val His Thr Gln Ile Arg Lys Thr Pro Leu Ala Gln Lys Lys Ala
76      165      170      175
78 cat ttg gct gaa atc caa ttg aac ggt ggt tcc atc tct gaa aag gtt 576
79 His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val
80      180      185      190
82 gac tgg gct cgt gaa cat ttc gaa aag act gtt gct gtc gac agc gtt 624
83 Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val
84      195      200      205
86 ttt gaa caa aac gaa atg att gac gct att gct gtc acc aag ggt cac 672
87 Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His
88      210      215      220
90 ggt ttc gaa ggt gtt acc cac aga tgg ggt act aag aaa ttg cca aga 720
91 Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg
92 225      230      235      240
94 aag act cac aga ggt cta aga aag gtt gct tgt att ggt gct tgg cat 768
95 Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Trp His
96      245      250      255
98 cca gcc cac gtt atg tgg agt gtt gcc aga gct ggt caa aga ggt tac 816
99 Pro Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr
100      260      265      270
102 cat tcc aga acc tcc att aac cac aag att tac aga gtc ggt aag ggt 864
103 His Ser Arg Thr Ser Ile Asn His Lys Ile Tyr Arg Val Gly Lys Gly
104      275      280      285
106 gat gat gaa gct aac ggt gct acc agc ttc gac aga acc aag aag act 912
107 Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr
108      290      295      300
110 att acc cca atg ggt ggt ttc gtc cac tac ggt gaa att aag aac gac 960
111 Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp
112 305      310      315      320
114 ttc atc atg gtt aaa ggt tgt atc cca ggt aac aga aag aga att gtt 1008
115 Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val
116      325      330      335
118 act ttg aga aag tct ttg tac acc aac act tct aga aag gct ttg gaa 1056
119 Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala Leu Glu
120      340      345      350
122 gaa gtc agc ttg aag tgg att gac act gct tct aag ttc ggt aag ggt 1104
123 Glu Val Ser Leu Lys Trp Ile Asp Thr Ala Ser Lys Phe Gly Lys Gly
124      355      360      365
126 aga ttc caa acc cca gct gaa aag cat gct ttc atg ggt act ttg aag 1152
127 Arg Phe Gln Thr Pro Ala Glu Lys His Ala Phe Met Gly Thr Leu Lys

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131 Lys Asp Leu
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144 Leu Pro Arg Lys Arg Ala Ala Ser Ile Arg Ala Arg Val Lys Ala Phe
145 20 25 30
147 Pro Lys Asp Asp Arg Ser Lys Pro Val Ala Leu Thr Ser Phe Leu Gly
148 35 40 45
150 Tyr Lys Ala Gly Met Thr Thr Ile Val Arg Asp Leu Asp Arg Pro Gly
151 50 55 60
153 Ser Lys Phe His Lys Arg Glu Val Val Glu Ala Val Thr Val Val Asp
154 65 70 75 80
156 Thr Pro Pro Val Val Val Gly Val Val Gly Tyr Val Glu Thr Pro
157 85 90 95
159 Arg Gly Leu Arg Ser Leu Thr Thr Val Trp Ala Glu His Leu Ser Asp
160 100 105 110
162 Glu Val Lys Arg Arg Phe Tyr Lys Asn Trp Tyr Lys Ser Lys Lys Lys
163 115 120 125
165 Ala Phe Thr Lys Tyr Ser Ala Lys Tyr Ala Gln Asp Gly Ala Gly Ile
166 130 135 140
168 Glu Arg Glu Leu Ala Arg Ile Lys Lys Tyr Ala Ser Val Val Arg Val
169 145 150 155 160
171 Leu Val His Thr Gln Ile Arg Lys Thr Pro Leu Ala Gln Lys Lys Ala
172 165 170 175
174 His Leu Ala Glu Ile Gln Leu Asn Gly Gly Ser Ile Ser Glu Lys Val
175 180 185 190
177 Asp Trp Ala Arg Glu His Phe Glu Lys Thr Val Ala Val Asp Ser Val
178 195 200 205
180 Phe Glu Gln Asn Glu Met Ile Asp Ala Ile Ala Val Thr Lys Gly His
181 210 215 220
183 Gly Phe Glu Gly Val Thr His Arg Trp Gly Thr Lys Lys Leu Pro Arg
184 225 230 235 240
186 Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly Ala Trp His
187 245 250 255
189 Pro Ala His Val Met Trp Ser Val Ala Arg Ala Gly Gln Arg Gly Tyr
190 260 265 270
192 His Ser Arg Thr Ser Ile Asn His Lys Ile Tyr Arg Val Gly Lys Gly
193 275 280 285
195 Asp Asp Glu Ala Asn Gly Ala Thr Ser Phe Asp Arg Thr Lys Lys Thr
196 290 295 300
198 Ile Thr Pro Met Gly Gly Phe Val His Tyr Gly Glu Ile Lys Asn Asp
199 305 310 315 320

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201 Phe Ile Met Val Lys Gly Cys Ile Pro Gly Asn Arg Lys Arg Ile Val
202             325             330             335
204 Thr Leu Arg Lys Ser Leu Tyr Thr Asn Thr Ser Arg Lys Ala Leu Glu
205             340             345             350
207 Glu Val Ser Leu Lys Trp Ile Asp Thr Ala Ser Lys Phe Gly Lys Gly
208             355             360             365
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211             370             375             380
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219 <211> LENGTH: 1170
220 <212> TYPE: DNA
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223 <220> FEATURE:
224 <221> NAME/KEY: CDS
225 <222> LOCATION: (1)..(1167)
227 <400> SEQUENCE: 3
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232 ctg ccc agg aag cgt gct gcc aga cac agg gga aag gtg aag gca ttc 96
233 Leu Pro Arg Lys Arg Ala Ala Arg His Arg Gly Lys Val Lys Ala Phe
234 20 25 30
236 cca aaa gat gat cca aac aag ccc tgc aag cta act gcc ttc ttg ggc 144
237 Pro Lys Asp Asp Pro Asn Lys Pro Cys Lys Leu Thr Ala Phe Leu Gly
238 35 40 45
240 tac aaa gct ggc atg act cac att gtc aga gat gtt gaa aaa cct gga 192
241 Tyr Lys Ala Gly Met Thr His Ile Val Arg Asp Val Glu Lys Pro Gly
242 50 55 60
244 tca aaa ctc cac aag aaa gag aca tgt gaa gct gtc acc atc att gaa 240
245 Ser Lys Leu His Lys Lys Glu Thr Cys Glu Ala Val Thr Ile Ile Glu
246 65 70 75 80
248 aca cct cca atg gtg att gtt ggt gtt gtt ggg tat gtg aag aca cct 288
249 Thr Pro Pro Met Val Ile Val Gly Val Val Gly Tyr Val Lys Thr Pro
250 85 90 95
252 cgt ggt ctt cgt tgc ctg aac act gtc tgg gct caa cat ctc agt gaa 336
253 Arg Gly Leu Arg Cys Leu Asn Thr Val Trp Ala Gln His Leu Ser Glu
254 100 105 110
256 gag ctt aag agg agg ttc tac aag aac tgg tgc aag tcc aag aag aag 384
257 Glu Leu Lys Arg Arg Phe Tyr Lys Asn Trp Cys Lys Ser Lys Lys Lys
258 115 120 125
260 gcc ttc ttg aaa tac tcc aag aaa tat gaa tct gat gaa ggg aaa aag 432
261 Ala Phe Leu Lys Tyr Ser Lys Lys Tyr Glu Ser Asp Glu Gly Lys Lys
262 130 135 140
264 gac atc cag aca cag ctg gag aaa ttg aag aag tat gca tgc gtc atc 480
265 Asp Ile Gln Thr Gln Leu Glu Lys Leu Lys Lys Tyr Ala Cys Val Ile
266 145 150 155 160
268 cgt gtt ttg gct cac act cag ata agg aag atg aag ggt ctg aaa cag 528

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269 Arg Val Leu Ala His Thr Gln Ile Arg Lys Met Lys Gly Leu Lys Gln
270          165          170          175
272 aag aaa gcc cat ttg atg gag ata cag gtg aat gga ggg aca att gct 576
273 Lys Lys Ala His Leu Met Glu Ile Gln Val Asn Gly Gly Thr Ile Ala
274          180          185          190
276 cag aag gtt gac ttt gca tat ggt ttc ttc gag aag cag gtt cca gtt 624
277 Gln Lys Val Asp Phe Ala Tyr Gly Phe Phe Glu Lys Gln Val Pro Val
278          195          200          205
280 gat gct gtt ttt cag aag gat gag atg att gac atc att ggt gtc acc 672
281 Asp Ala Val Phe Gln Lys Asp Glu Met Ile Asp Ile Ile Gly Val Thr
282          210          215          220
284 aag ggt aag ggt tat gaa ggt gtt gta act cgt tgg ggt gtg aca cgt 720
285 Lys Gly Lys Gly Tyr Glu Gly Val Val Thr Arg Trp Gly Val Thr Arg
286 225          230          235          240
288 ctt cct cgc aaa acc cac agg ggt ctg cgt aag gtt gct tgt att gga 768
289 Leu Pro Arg Lys Thr His Arg Gly Leu Arg Lys Val Ala Cys Ile Gly
290          245          250          255
292 gcc tgg cac cct gct aga gtt tcc tac aca gtt gcc cgt gct ggt caa 816
293 Ala Trp His Pro Ala Arg Val Ser Tyr Thr Val Ala Arg Ala Gly Gln
294          260          265          270
296 aat gga tac cat cac cgt acc gag atg aac aag aag gtt tac aaa cta 864
297 Asn Gly Tyr His His Arg Thr Glu Met Asn Lys Lys Val Tyr Lys Leu
298          275          280          285
300 ggg aag gct ggc caa gag tcc cat gct gct gta act gat ttt gac agg 912
301 Gly Lys Ala Gly Gln Glu Ser His Ala Ala Val Thr Asp Phe Asp Arg
302          290          295          300
304 acc gag aaa gac att act ccc atg ggt gga ttt ccc cat tat ggt gtg 960
305 Thr Glu Lys Asp Ile Thr Pro Met Gly Gly Phe Pro His Tyr Gly Val
306 305          310          315          320
308 gtg aag gat gat tac ctg ttg atc aag gga tgc tgt gtt ggt cct aag 1008
309 Val Lys Asp Asp Tyr Leu Leu Ile Lys Gly Cys Cys Val Gly Pro Lys
310          325          330          335
312 aag agg gtt gta acc ctt cgt cag tcc ctg ctc aac cag acc tct cgt 1056
313 Lys Arg Val Val Thr Leu Arg Gln Ser Leu Leu Asn Gln Thr Ser Arg
314          340          345          350
316 gtc gct ctt gag gag att aag ctg aag ttc atc gat aca tcc tca aag 1104
317 Val Ala Leu Glu Glu Ile Lys Leu Lys Phe Ile Asp Thr Ser Ser Lys
318          355          360          365
320 ttt gga cat ggt cgc ttc cag acc act caa gag aag cag aaa ttc tat 1152
321 Phe Gly His Gly Arg Phe Gln Thr Thr Gln Glu Lys Gln Lys Phe Tyr
322          370          375          380
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329 <210> SEQ ID NO: 4
330 <211> LENGTH: 389
331 <212> TYPE: PRT
332 <213> ORGANISM: Nicotiana tabacum
334 <400> SEQUENCE: 4

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VERIFICATION SUMMARY

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